SEQUENCE LISTING

<110> Suntory Limited

<120> Screening method for genes of brewing yeast

<130> S07F1263

<160> 32

<210> 1

<211> 1377

<212> DNA

<213> Saccharomyces sp.

<400> 1

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ctgaggatat gctcgtacat catgtttgcc attacatgtt tgatttcat ctctgtacag   180
gcgctgcagc ttttgcacat ggtcatctat atcaaagaaa aaagctttag agattacttc   240
aatgaatatt tcagaagtct gaagtacaat ttattttggg gtacttatcc catgggatta   300
gtaacaatca taaatttttt gggggcgctg tcacaaaaat ttaccacgac aagccctgcg   360
aatgccaagc acttgatcat ttttgtttac gtcctgtggt ggtatgacct cgcggtttgt   420
ttagtaaccg cttgggggat ttcattcctc atctggcaaa agtactactt cgtggacggg   480
gttggaaatc actcttcata cagttcacga atggcttccg accacatgaa aagcgtactg   540
ttgctagata tcattccgct ggtcgttgtc gcttcgagcg gtgggacatt tacaatgtca   600
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ctttacatca ataagatacc accaatgacg caggtattta cgttgttctt ggtattgggg    780

ccattgggcc aaggaagttt tggtattttg ttgcttactg acaatataag aaagtatgta    840

gaaaaatact acccaaggga aaacatcacc atggaacaag aaatactaac cattatggtt    900

ccgtggtgtt tcaaggttct gggcatgaca tttgctttgg cattaatcgc tatgggttac    960

ttctttacgg taatttccct tatttcgatt ttatcatact acaatgaaag agttgttgac   1020

aatgaaacag gcaaagtgaa aaggatctac actttccata aaggtttctg ggggatgact   1080

ttcccgatgg gtaccatgtc tttgggaaac gaggagctgt atctgcaata caaccagtat   1140

gttcccttat atgcattcag agtcatagct accatatatg gtggtatttg tgtttgctgg   1200

tcaatcttat gcctctcgtg cacgttgtat ggttacctga aaacgattct ccatgctgcc   1260

cgtaaacctt cgttttatc agaggaaggg acggagaaga ctgtcaattc tcctttcaac   1320

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<213> Saccharomyces sp.

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gcttgtgcac tggaacaatt actgcttcaa aaaaacttat ctgcttatag gttagatggt    180

gataacattc gttttggttt gaataaggat ttgggcttct cagaaaagga cagaaatgaa    240

aacattcgta gaattagtga agtatccaag ctattcgctg attcgtgtgc tgtatccatc    300

acttcattta tttccccata cagagtcgat agagacagag cccgtgattt acataaggaa    360

gcaggcttga agttcattga aatttttgtt gatgttccat tagaagtcgc tgagcaaaga    420

gaccctaagg gtttgtataa gaaagccaga gaaggtgtga ttaaagagtt cactggtatt    480
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tcagctcctt acgaagctcc aaaggcccca gagttgcatt taagaactga ccaaaagact 540

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<210> 3

<211> 458

<212> PRT

<213> Saccharomyces sp.

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Phe Met Phe Val Met Val Met Gly Val Gly Ile Ser Ser Asn Ile
                 20   25   30

Leu Tyr Ser Phe Pro Tyr Pro Ala Arg Trp Leu Arg Ile Cys Ser
                 35   40   45

Tyr Ile Met Phe Ala Ile Thr Cys Leu Ile Phe Ile Ser Val Gln
                 50   55   60

Ala Leu Gln Leu Leu His Met Val Ile Tyr Ile Lys Glu Lys Ser
                 65   70   75

Phe Arg Asp Tyr Phe Asn Glu Tyr Phe Arg Ser Leu Lys Tyr Asn
                 80   85   90

Leu Phe Trp Gly Thr Tyr Pro Met Gly Leu Val Thr Ile Ile Asn
                 95   100   105

Phe Leu Gly Ala Leu Ser Gln Lys Phe Thr Thr Thr Ser Pro Ala
                110   115   120

Asn Ala Lys His Leu Ile Ile Phe Val Tyr Val Leu Trp Trp Tyr
      125   130   135

Asp Leu Ala Val Cys Leu Val Thr Ala Trp Gly Ile Ser Phe Leu
      140   145   150

Ile Trp Gln Lys Tyr Tyr Phe Val Asp Gly Val Gly Asn His Ser
      155   160   165

Ser Tyr Ser Ser Arg Met Ala Ser Asp His Met Lys Ser Val Leu
      170   175   180

Leu Leu Asp Ile Ile Pro Leu Val Val Val Ala Ser Ser Gly Gly
      185   190   195

Thr Phe Thr Met Ser Lys Ile Phe Gly Thr Thr Phe Asp Arg Asn
      200   205   210

Ile Gln Leu Leu Thr Leu Val Ile Cys Ala Leu Val Trp Leu His
      215   220   225

Ala Leu Ile Phe Val Phe Ile Leu Ile Thr Ile Tyr Phe Trp Asn
      230   235   240

Leu Tyr Ile Asn Lys Ile Pro Pro Met Thr Gln Val Phe Thr Leu
      245   250   255

Phe Leu Val Leu Gly Pro Leu Gly Gln Gly Ser Phe Gly Ile Leu
      260   265   270

Leu Leu Thr Asp Asn Ile Arg Lys Tyr Val Glu Lys Tyr Tyr Pro
      275   280   285

Arg Glu Asn Ile Thr Met Glu Gln Glu Ile Leu Thr Ile Met Val
      290   295   300

Pro Trp Cys Phe Lys Val Leu Gly Met Thr Phe Ala Leu Ala Leu
      305   310   315

Ile Ala Met Gly Tyr Phe Phe Thr Val Ile Ser Leu Ile Ser Ile
      320   325   330

Leu Ser Tyr Tyr Asn Glu Arg Val Val Asp Asn Glu Thr Gly Lys

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Val Lys Arg Ile Tyr Thr Phe His Lys Gly Phe Trp Gly Met Thr
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Phe Pro Met Gly Thr Met Ser Leu Gly Asn Glu Glu Leu Tyr Leu
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Gln Tyr Asn Gln Tyr Val Pro Leu Tyr Ala Phe Arg Val Ile Ala
                    380                 385                 390
Thr Ile Tyr Gly Gly Ile Cys Val Cys Trp Ser Ile Leu Cys Leu
                    395                 400                 405
Ser Cys Thr Leu Tyr Gly Tyr Leu Lys Thr Ile Leu His Ala Ala
                    410                 415                 420
Arg Lys Pro Ser Phe Leu Ser Glu Glu Gly Thr Glu Lys Thr Val
                    425                 430                 435
Asn Ser Pro Phe Asn Ser Ile Glu Ser Val Glu Glu Ser Asn Ser
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Ala Ile Asp Ser Thr Tyr Leu Thr
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<211> 202

<212> PRT

<213> Saccharomyces sp.

<400> 4

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Gly Leu Ser Ala Ser Gly Lys Ser Thr Ile Ala Cys Ala Leu Glu
                35   40   45

Gln Leu Leu Leu Gln Lys Asn Leu Ser Ala Tyr Arg Leu Asp Gly
                50   55   60

Asp Asn Ile Arg Phe Gly Leu Asn Lys Asp Leu Gly Phe Ser Glu
                65   70   75

Lys Asp Arg Asn Glu Asn Ile Arg Arg Ile Ser Glu Val Ser Lys
                80   85   90

Leu Phe Ala Asp Ser Cys Ala Val Ser Ile Thr Ser Phe Ile Ser
                95   100   105

Pro Tyr Arg Val Asp Arg Asp Arg Ala Arg Asp Leu His Lys Glu
                110   115   120

Ala Gly Leu Lys Phe Ile Glu Ile Phe Val Asp Val Pro Leu Glu
                125   130   135

Val Ala Glu Gln Arg Asp Pro Lys Gly Leu Tyr Lys Lys Ala Arg
                140   145   150

Glu Gly Val Ile Lys Glu Phe Thr Gly Ile Ser Ala Pro Tyr Glu
                155   160   165

Ala Pro Lys Ala Pro Glu Leu His Leu Arg Thr Asp Gln Lys Thr
                170   175   180

Val Glu Glu Cys Ala Ala Ile Ile Tyr Glu Tyr Leu Val Asn Glu
                185   190   195

Lys Ile Ile Arg Lys His Leu
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<211> 15

<212> Artificial sequence

<213> M13_for

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<210> 6

<211> 17

<212> Artificial sequence

<213> M13_rv

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<210> 7

<211> 22

<212> Artificial sequence

<213> SS-cosF.1

<400> 7

aggcgtatca cgaggccctt tc   22

<210> 8

<211> 29

<212> Artificial sequence

<213> SS-cosR.1

<400> 8

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<211> 36

<212> Artificial sequence

<213> XVI-1(L)cer-95894

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cgcaagctcc gtacgttcaa cattcttatg aacggc   36

<210> 10

<211> 36

<212> Artificial sequence

<213> XVI-1(R)nonSc-106302rv

<400> 10

gcatcatcgt cgtgatcctt ctttggcaaa tgcagg   36

<210> 11

<211> 36

<212> Artificial sequence

<213> XVI-2(L)cer-859737

<400> 11

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<210> 12

<211> 35

<212> Artificial sequence

<213> XVI-2(R)nonSc-864595rv

<400> 12

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<210> 13

<211> 26

<212> Artificial sequence

<213> SacI-nonScSSU1_for1

<400> 13

gagctcatgg tcgctagttg gatgct   26

<210> 14

<211> 26

<212> Artificial sequence

<213> BglII-nonScSSU1_rv1460

<400> 14

agatctcagc ttcagcccaa tccatt   26

<210> 15

<211> 26

<212> Artificial sequence

<213> SacI-ScSSU1_for1

<400> 15

gagctcatgg ttgccaattg ggtact   26

<210> 16

<211> 26

<212> Artificial sequence

<213> BglII-ScSSU1_rv1406

<400> 16

agatctctcc tacatgaaat gcttgc   26

<210> 17

<211> 120

<212> Artificial sequence

<213> nonScSSU1_for

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ctgtacagct gtttgtcatg gttatggggg tcggtatttc ccttgacagt cttgacgtgc   120

<210> 18

<211> 120

<212> Artificial sequence

<213> nonScSSU1_rv

<400> 18

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<210> 19

<211> 120

<212> Artificial sequence

<213> ScSSU1_for

<400> 19

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<210> 20

<211> 120

<212> Artificial sequence

<213> ScSSU1_rv

<400> 20

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<210> 21

<211> 120

<212> Artificial sequence

<213> nonScSSU1_for+pGAPAUR

<400> 21

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<210> 22

<211> 120

<212> Artificial sequence

<213> nonScSSU1_rv+AUR1-C

<400> 22

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<210> 23

<211> 20

<212> Artificial sequence

<213> ScSSU1_for331

<400> 23

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<210> 24

<211> 21

<212> Artificial sequence

<213> ScSSU1_982rv

<400> 24

cgacagaaat cacggtgaaa a   21

<210> 25

<211> 22

<212> Artificial sequence

<213> nonScSSU1_329

<400> 25

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<210> 26

<211> 22

<212> Artificial sequence

<213> nonScSSU1_981rv

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<213> PDA1_for1

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<212> Artificial sequence

<213> PDA1_730rv

<400> 28

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<210> 29

<211> 33

<212> Artificial sequence

<213> SacI-nonSc-MET14_for-21

<400> 29

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<210> 30

<211> 30

<212> Artificial sequence

<213> BamHI-nonSc-MET14_rv618

<400> 30

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<210> 31

<211> 33

<212> Artificial sequence

<213> SacI-ScMET14_for

<400> 31

ctcgagctca gaaaagttgg aattatttct cca   33

<210> 32

<211> 30

<212> Artificial sequence

<213> BamHI-ScMET14_rv

<400> 32

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